EXHIBIT 7

EXHIBIT 7

NCBI **Blast 2 Sequences results**

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix [BLOSUM62 ▼] gap open: [11] gap extension: [1]

x_dropoff: [50] expect: [10.0000] wordsize: [3] Filter ☐ View option [Standard ▼]

Masking character option [X for protein, n for nucleotide ▼]   Masking color option [Black ▼]

☐ Show CDS translation [Align]

Sequence 1: gi|6678678|ref|NP_032519.1|leptin [Mus musculus] >gi|730219|sp|P41160|LEP_MOUSE Leptin precursor (Obesity factor) >gi|603288|gb|AAA64564.1| ob >gi|726297|gb|AAA64213.1| obesity protein >gi|26326917|dbj|BAC27202.1| unnamed protein product [Mus musculus] >gi|74216350|dbj|BAE25117.1| unnamed protein product [Mus musculus] >gi|115545388|gb|AAI25246.1| Leptin {Mus musculus] >gi|1092655|prf||2024338A obeser gene Length = 167 (1 .. 167)

Sequence 2: gi|2406650|gb|AAC60368.1|leptin [Gallus gallus] >gi|3024234|sp|O42164|LEP_CHICK Leptin precursor (Obesity factor) >gi|3435282|gb|AAC32380.1| leptin precursor [Gallus gallus] Length = 163 (1 .. 163)
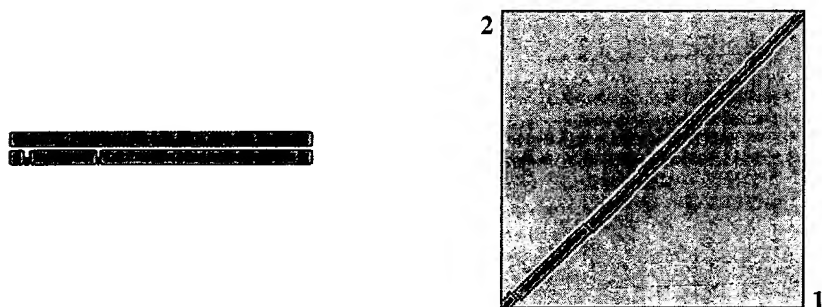
NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score =  301 bits (770),  Expect = 1e-80
 Identities = 158/167 (94%),  Positives = 159/167 (95%),  Gaps = 4/167 (2%)

Query  1    MCWRPLCRFLWLWSYLSYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSAKQRVTGL  60
            MCWRPLCR   LWSYL YVQAVP Q  QDDTKTLIKTIVTRINDISHT SVSAKQRVTGL
Sbjct  1    MCWRPLCR---LWSYLVYVQAVPCQIFQDDTKTLIKTIVTRINDISHT-SVSAKQRVTGL  56

Query  61   DFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLP  120
            DFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLP
Sbjct  57   DFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLP  116

Query  121  QTSGLQKPESLDGVLEASLYSTEVVALSRLQGSLQDILQQLDVSPEC  167
            QTSGLQKPESLDGVLEASLYSTEVVALSRLQGSLQDILQQLD+SPEC
Sbjct  117  QTSGLQKPESLDGVLEASLYSTEVVALSRLQGSLQDILQQLDISPEC  163
```

```
CPU time:      0.02 user secs.        0.01 sys. secs        0.03 total secs.
```

```
Lambda      K        H
   0.319    0.133    0.387

Gapped
Lambda      K        H
   0.267    0.0410   0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 312
Number of extensions: 119
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 167
Length of database: 1,565,033,500
Length adjustment: 124
Effective length of query: 43
Effective length of database: 1,565,033,376
Effective search space: 67296435168
Effective search space used: 67296435168
Neighboring words threshold: 9
X1: 16 ( 7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 73 (32.7 bits)
```